Table S2. Validation of genome-wide SNPs by array.

Cultivar	Matched	Mismatched	Total
Omachi	535	0	535
Yamadanishiki	384	0	384
Kameji	296	0	296
Gohyakumangoku	316	0	316
Koshihikari	184	0	184
Norin8	152	1	153
Moroberekan	220	1	221

Genomic DNAs of each cultivar and Nipponbare were analysed using SNP arrays by using the Illumina Bead Station 500G system. Omachi, Yamadanishiki, Kameji, Gohyakumangoku, Koshihikari, and Norin 8 were analyzed using a set of SNPs that was selected from SNP resources developed on the basis of Omachi and Nippobare. Moroberekan was analyzed using a set of SNPs that was selected from SNP resources developed on the basis of *japonica* rice cultivars.